GCGGACGCGT GGGTGAAATT GAAAATCAAG ATAAAAATGT TCACAATTAA 50

GCTCCTTCTT TTTATTGTTC CTCTAGTTAT TTCCTCCAGA ATTGATCAAG 100

ACAATTCATC ATTTGATTCT CTATCTCCAG AGCCAAAATC AAGATTTGCT 150

ATGTTAGACG ATGTAAAAAT TTTAGCCAAT GGCCTCCTTC AGTTGGGACA 200

TGGTCTTAAA GACTTTGTCC ATAAGACGAA GGGCCAAATT AATGACATAT 250

TTCAAAAACT CAACATATTT GATCAGTCTT TTTATGATCT ATCGCTGCAA 300

ACCAGTGAAA TCAAAGAAGA AGAAAAGGAA CTGAGAAGAA CTACATATAA 350

ACTACAAGTC AAAAATGAAG AGGTAAAGAA TATGTCACTT GAACTCAACT 400

CAAAACTTGA AAGCCTCCTA GAAGAAAAAA TTCTACTTCA ACAAAAAGTG 450

AAATATTTAG AAGAGCAACT AACTAACTTA ATTCAAAATC AACCTGAAAC 500

TCCAGAACAC CCAGAAGTAA CTTCACTTAA AACTTTTGTA GAAAAACAAG 550

ATAATAGCAT CAAAGACCTT CTCCAGACCG TGGAAGACCA ATATAAACAA 600

TTAAACCAAC AGCATAGTCA AATAAAAGAA ATAGAAAATC AGCTCAGAAG 650

GACTAGTATT CAAGAACCCA CAGAAATTTC TCTATCTTCC AAGCCAAGAG 700

CACCAAGAAC TACTCCCTTT CTTCAGTTGA ATGAAATAAG AAATGTAAAA 750

CATGATGGCA TTCCTGCTGA ATGTACCACC ATTTATAACA GAGGTGAACA 800

TACAAGTGGC ATGTATGCCA TCAGACCCAG CAACTCTCAA GTTTTTCATG 850

TCTACTGTGA TGTTATATCA GGTAGTCCAT GGACATTAAT TCAACATCGA 900

ATAGATGGAT CACAAAACTT CAATGAAACG TGGGAGAACT ACAAATATGG 950

TTTTGGGAGG CTTGATGGAG AATTTTGGTT GGGCCTAGAG AAGATATACT 1000

CCATAGTGAA GCAATCTAAT TATGTTTTAC GAATTGAGTT GGAAGACTGG 1050

AAAGACAACA AACATTATAT TGAATATTCT TTTTACTTGG GAAATCACGA 1100

AACCAACTAT ACGCTACATC TAGTTGCGAT TACTGGCAAT GTCCCCAATG 1150

CAATCCCGGA AAACAAAGAT TTGGTGTTTT CTACTTGGGA TCACAAAGCA 1200

AAAGGACACT TCAACTGTCC AGAGGGTTAT TCAGGAGGCT GGTGGTGGCA 1250

TGATGAGTGT GGAGAAAACA ACCTAAATGG TAAATATAAC AAACCAAGAG 1300

CAAAATCTAA GCCAGAGAGG AGAAGAGGAT TATCTTGGAA GTCTCAAAAT 1350

GGAAGGTTAT ACTCTATAAA ATCAACCAAA ATGTTGATCC ATCCAACAGA 1400

TTCAGAAAGC TTTGAATGAA CTGAGGCAAT TTAAAGGCAT ATTTAACCAT 1450

Figure 1-A

TAACTCATTC CAAGTTAATG TGGTCTAATA ATCTGGTATA AATCCTTAAG 1500
AGAAAGCTTG AGAAATAGAT TTTTTTTATC TTAAAGTCAC TGTCTATTTA 1550
AGATTAAACA TACAATCACA TAACCTTAAA GAATACCGTT TACATTTCTC 1600
AATCAAAATT CTTATAATAC TATTTGTTTT AAATTTTGTG ATGTGGGAAT 1650
CAATTTTAGA TGGTCACAAT CTAGATTATA ATCAATAGGT GAACTTATTA 1700
AATAACTTTT CTAAATAAAA AATTTAGAGA CTTTTATTTT AAAAGGCATC 1750
ATATGAGCTA ATATCACAAC TTTCCCAGTT TAAAAAACTA GTACTCTTGT 1800
TAAAACTCTA AACTTGACTA AATACAGAGG ACTGGTAATT GTACAGTTCT 1850
TAAATGTTGT AGTATTAATT TCAAAACTAA AAATCGTCAG CACAGAGTAT 1900
GTGTAAAAAT CTGTAATACA AATTTTTAAA CTGATGCTTC ATTTTGCTAC 1950
AAAATAATTT GGAGTAAATG TTTGATATGA TTTATTTATG AAACCTAATG 2000
AAGCAGAATT AAATACTGTA TTAAAATAAG TTCGCTGTCT TT 2042

Figure 1-A

```
Met Phe Thr Ile Lys Leu Leu Leu Phe Ile Val Pro Leu Val Ile
 1               5                  10                  15

Ser Ser Arg Ile Asp Gln Asp Asn Ser Ser Phe Asp Ser Leu Ser
            20                  25                  30

Pro Glu Pro Lys Ser Arg Phe Ala Met Leu Asp Asp Val Lys Ile
            35                  40                  45

Leu Ala Asn Gly Leu Leu Gln Leu Gly His Gly Leu Lys Asp Phe
            50                  55                  60

Val His Lys Thr Lys Gly Gln Ile Asn Asp Ile Phe Gln Lys Leu
            65                  70                  75

Asn Ile Phe Asp Gln Ser Phe Tyr Asp Leu Ser Leu Gln Thr Ser
            80                  85                  90

Glu Ile Lys Glu Glu Glu Lys Glu Leu Arg Arg Thr Thr Tyr Lys
            95                 100                 105

Leu Gln Val Lys Asn Glu Glu Val Lys Asn Met Ser Leu Glu Leu
           110                 115                 120

Asn Ser Lys Leu Glu Ser Leu Leu Glu Glu Lys Ile Leu Leu Gln
           125                 130                 135

Gln Lys Val Lys Tyr Leu Glu Glu Gln Leu Thr Asn Leu Ile Gln
           140                 145                 150

Asn Gln Pro Glu Thr Pro Glu His Pro Glu Val Thr Ser Leu Lys
           155                 160                 165

Thr Phe Val Glu Lys Gln Asp Asn Ser Ile Lys Asp Leu Leu Gln
           170                 175                 180

Thr Val Glu Asp Gln Tyr Lys Gln Leu Asn Gln Gln His Ser Gln
           185                 190                 195

Ile Lys Glu Ile Glu Asn Gln Leu Arg Arg Thr Ser Ile Gln Glu
           200                 205                 210

Pro Thr Glu Ile Ser Leu Ser Ser Lys Pro Arg Ala Pro Arg Thr
           215                 220                 225

Thr Pro Phe Leu Gln Leu Asn Glu Ile Arg Asn Val Lys His Asp
           230                 235                 240

Gly Ile Pro Ala Glu Cys Thr Thr Ile Tyr Asn Arg Gly Glu His
           245                 250                 255

Thr Ser Gly Met Tyr Ala Ile Arg Pro Ser Asn Ser Gln Val Phe
           260                 265                 270

His Val Tyr Cys Asp Val Ile Ser Gly Ser Pro Trp Thr Leu Ile
           275                 280                 285
```

Figure 1-B

```
Gln His Arg Ile Asp Gly Ser Gln Asn Phe Asn Glu Thr Trp Glu
                290                 295                 300

Asn Tyr Lys Tyr Gly Phe Gly Arg Leu Asp Gly Glu Phe Trp Leu
                305                 310                 315

Gly Leu Glu Lys Ile Tyr Ser Ile Val Lys Gln Ser Asn Tyr Val
                320                 325                 330

Leu Arg Ile Glu Leu Glu Asp Trp Lys Asp Asn Lys His Tyr Ile
                335                 340                 345

Glu Tyr Ser Phe Tyr Leu Gly Asn His Glu Thr Asn Tyr Thr Leu
                350                 355                 360

His Leu Val Ala Ile Thr Gly Asn Val Pro Asn Ala Ile Pro Glu
                365                 370                 375

Asn Lys Asp Leu Val Phe Ser Thr Trp Asp His Lys Ala Lys Gly
                380                 385                 390

His Phe Asn Cys Pro Glu Gly Tyr Ser Gly Gly Trp Trp Trp His
                395                 400                 405

Asp Glu Cys Gly Glu Asn Asn Leu Asn Gly Lys Tyr Asn Lys Pro
                410                 415                 420

Arg Ala Lys Ser Lys Pro Glu Arg Arg Arg Gly Leu Ser Trp Lys
                425                 430                 435

Ser Gln Asn Gly Arg Leu Tyr Ser Ile Lys Ser Thr Lys Met Leu
                440                 445                 450

Ile His Pro Thr Asp Ser Glu Ser Phe Glu
                455                 460
```

Figure 1-B Page 2 of 2

GGCTGAGGGG AGGCCCGGAG CCTTTCTGGG GCCTGGGGGA TCCTCTTGCA 50

CTGGTGGGTG GAGAGAAGCG CCTGCAGCCA ACCAGGGTCA GGCTGTGCTC 100

ACAGTTTCCT CTGGCGGCAT GTAAAGGCTC CACAAAGGAG TTGGGAGTTC 150

AAATGAGGCT GCTGCGGACG GCCTGAGGAT GGACCCCAAG CCCTGGACCT 200

GCCGAGCGTG GCACTGAGGC AGCGGCTGAC GCTACTGTGA GGGAAAGAAG 250

GTTGTGAGCA GCCCCGCAGG ACCCCTGGCC AGCCCTGGCC CCAGCCTCTG 300

CCGGAGCCCT CTGTGGAGGC AGAGCCAGTG GAGCCCAGTG AGGCAGGGCT 350

GCTTGGCAGC CACCGGCCTG CAACTCAGGA ACCCCTCCAG AGGCCATGGA 400

CAGGCTGCCC CGCTGACGGC CAGGGTGAAG CATGTGAGGA GCCGCCCCGG 450

AGCCAAGCAG GAGGGAAGAG GCTTTCATAG ATTCTATTCA CAAAGAATAA 500

CCACCATTTT GCAAGGACCA TGAGGCCACT GTGCGTGACA TGCTGGTGGC 550

TCGGACTGCT GGCTGCCATG GGAGCTGTTG CAGGCCAGGA GGACGGTTTT 600

GAGGGCACTG AGGAGGGCTC GCCAAGAGAG TTCATTTACC TAAACAGGTA 650

CAAGCGGGCG GGCGAGTCCC AGGACAAGTG CACCTACACC TTCATTGTGC 700

CCCAGCAGCG GGTCACGGGT GCCATCTGCG TCAACTCCAA GGAGCCTGAG 750

GTGCTTCTGG AGAACCGAGT GCATAAGCAG GAGCTAGAGC TGCTCAACAA 800

TGAGCTGCTC AAGCAGAAGC GGCAGATCGA GACGCTGCAG CAGCTGGTGG 850

AGGTGGACGG CGGCATTGTG AGCGAGGTGA AGCTGCTGCG CAAGGAGAGC 900

CGCAACATGA ACTCGCGGGT CACGCAGCTC TACATGCAGC TCCTGCACGA 950

GATCATCCGC AAGCGGGACA ACGCGTTGGA GCTCTCCCAG CTGGAGAACA 1000

GGATCCTGAA CCAGACAGCC GACATGCTGC AGCTGGCCAG CAAGTACAAG 1050

GACCTGGAGC ACAAGTACCA GCACCTGGCC ACACTGGCCC ACAACCAATC 1100

AGAGATCATC GCGCAGCTTG AGGAGCACTG CCAGAGGGTG CCCTCGGCCA 1150

GGCCCGTCCC CCAGCCACCC CCCGCTGCCC CGCCCCGGGT CTACCAACCA 1200

CCCACCTACA ACCGCATCAT CAACCAGATC TCTACCAACG AGATCCAGAG 1250

TGACCAGAAC CTGAAGGTGC TGCCACCCCC TCTGCCCACT ATGCCCACTC 1300

TCACCAGCCT CCCATCTTCC ACCGACAAGC CGTCGGGCCC ATGGAGAGAC 1350

TGCCTGCAGG CCCTGGAGGA TGGCCACGAC ACCAGCTCCA TCTACCTGGT 1400

GAAGCCGGAG AACACCAACC GCCTCATGCA GGTGTGGTGC GACCAGAGAC 1450

Figure 2 Page 1 of 2

ACGACCCCGG GGGCTGGACC GTCATCCAGA GACGCCTGGA TGGCTCTGTT 1500

AACTTCTTCA GGAACTGGGA GACGTACAAG CAAGGGTTTG GGAACATTGA 1550

CGGCGAATAC TGGCTGGGCC TGGAGAACAT TTACTGGCTG ACGAACCAAG 1600

GCAACTACAA ACTCCTGGTG ACCATGGAGG ACTGGTCCGG CCGCAAAGTC 1650

TTTGCAGAAT ACGCCAGTTT CCGCCTGGAA CCTGAGAGCG AGTATTATAA 1700

GCTGCGGCTG GGGCGCTACC ATGGCAATGC GGGTGACTCC TTTACATGGC 1750

ACAACGGCAA GCAGTTCACC ACCCTGGACA GAGATCATGA TGTCTACACA 1800

GGAAACTGTG CCCACTACCA GAAGGGAGGC TGGTGGTATA ACGCCTGTGC 1850

CCACTCCAAC CTCAACGGGG TCTGGTACCG CGGGGGCCAT TACCGGAGCC 1900

GCTACCAGGA CGGAGTCTAC TGGGCTGAGT TCCGAGGAGG CTCTTACTCA 1950

CTCAAGAAAG TGGTGATGAT GATCCGACCG AACCCCAACA CCTTCCACTA 2000

AGCCAGCTCC CCCTCCTGAC CTCTCGTGGC CATTGCCAGG AGCCCACCCT 2050

GGTCACGCTG GCCACAGCAC AAAGAACAAC TCCTCACCAG TTCATCCTGA 2100

GGCTGGGAGG ACCGGGATGC TGGATTCTGT TTTCCGAAGT CACTGCAGCG 2150

GATGATGGAA CTGAATCGAT ACGGTGTTTT CTGTCCCTCC TACTTTCCTT 2200

CACACCAGAC AGCCCCTCAT GTCTCCAGGA CAGGACAGGA CTACAGACAA 2250

CTCTTTCTTT AAATAAATTA AGTCTCTACA ATAAAAAAAA 2290

```
Met Arg Pro Leu Cys Val Thr Cys Trp Trp Leu Gly Leu Leu Ala
  1               5                  10                  15

Ala Met Gly Ala Val Ala Gly Gln Glu Asp Gly Phe Glu Gly Thr
            20                  25                  30

Glu Glu Gly Ser Pro Arg Glu Phe Ile Tyr Leu Asn Arg Tyr Lys
            35                  40                  45

Arg Ala Gly Glu Ser Gln Asp Lys Cys Thr Tyr Thr Phe Ile Val
            50                  55                  60

Pro Gln Gln Arg Val Thr Gly Ala Ile Cys Val Asn Ser Lys Glu
            65                  70                  75

Pro Glu Val Leu Leu Glu Asn Arg Val His Lys Gln Glu Leu Glu
            80                  85                  90

Leu Leu Asn Asn Glu Leu Leu Lys Gln Lys Arg Gln Ile Glu Thr
            95                  100                 105

Leu Gln Gln Leu Val Glu Val Asp Gly Gly Ile Val Ser Glu Val
            110                 115                 120

Lys Leu Leu Arg Lys Glu Ser Arg Asn Met Asn Ser Arg Val Thr
            125                 130                 135

Gln Leu Tyr Met Gln Leu Leu His Glu Ile Ile Arg Lys Arg Asp
            140                 145                 150

Asn Ala Leu Glu Leu Ser Gln Leu Glu Asn Arg Ile Leu Asn Gln
            155                 160                 165

Thr Ala Asp Met Leu Gln Leu Ala Ser Lys Tyr Lys Asp Leu Glu
            170                 175                 180

His Lys Tyr Gln His Leu Ala Thr Leu Ala His Asn Gln Ser Glu
            185                 190                 195

Ile Ile Ala Gln Leu Glu Glu His Cys Gln Arg Val Pro Ser Ala
            200                 205                 210

Arg Pro Val Pro Gln Pro Pro Pro Ala Ala Pro Pro Arg Val Tyr
            215                 220                 225

Gln Pro Pro Thr Tyr Asn Arg Ile Ile Asn Gln Ile Ser Thr Asn
            230                 235                 240

Glu Ile Gln Ser Asp Gln Asn Leu Lys Val Leu Pro Pro Pro Leu
            245                 250                 255

Pro Thr Met Pro Thr Leu Thr Ser Leu Pro Ser Ser Thr Asp Lys
            260                 265                 270

Pro Ser Gly Pro Trp Arg Asp Cys Leu Gln Ala Leu Glu Asp Gly
            275                 280                 285
```

Figure 3

```
His Asp Thr Ser Ser Ile Tyr Leu Val Lys Pro Glu Asn Thr Asn
                290                 295                 300

Arg Leu Met Gln Val Trp Cys Asp Gln Arg His Asp Pro Gly Gly
                305                 310                 315

Trp Thr Val Ile Gln Arg Arg Leu Asp Gly Ser Val Asn Phe Phe
                320                 325                 330

Arg Asn Trp Glu Thr Tyr Lys Gln Gly Phe Gly Asn Ile Asp Gly
                335                 340                 345

Glu Tyr Trp Leu Gly Leu Glu Asn Ile Tyr Trp Leu Thr Asn Gln
                350                 355                 360

Gly Asn Tyr Lys Leu Leu Val Thr Met Glu Asp Trp Ser Gly Arg
                365                 370                 375

Lys Val Phe Ala Glu Tyr Ala Ser Phe Arg Leu Glu Pro Glu Ser
                380                 385                 390

Glu Tyr Tyr Lys Leu Arg Leu Gly Arg Tyr His Gly Asn Ala Gly
                395                 400                 405

Asp Ser Phe Thr Trp His Asn Gly Lys Gln Phe Thr Thr Leu Asp
                410                 415                 420

Arg Asp His Asp Val Tyr Thr Gly Asn Cys Ala His Tyr Gln Lys
                425                 430                 435

Gly Gly Trp Trp Tyr Asn Ala Cys Ala His Ser Asn Leu Asn Gly
                440                 445                 450

Val Trp Tyr Arg Gly Gly His Tyr Arg Ser Arg Tyr Gln Asp Gly
                455                 460                 465

Val Tyr Trp Ala Glu Phe Arg Gly Gly Ser Tyr Ser Leu Lys Lys
                470                 475                 480

Val Val Met Met Ile Arg Pro Asn Pro Asn Thr Phe His
                485                 490         493
```

Figure 3 Page 2 of 2

GCAGCTGGTT ACTGCATTTC TCCATGTGGC AGACAGAGCA AAGCCACAAC 50

GCTTTCTCTG CTGGATTAAA GACGGCCCAC AGACCAGAAC TTCCACTATA 100

CTACTTAAAA TTACATAGGT GGCTTGTCAA ATTCAATTGA TTAGTATTGT 150

AAAAGGAAAA AGAAGTTCCT TCTTACAGCT TGGATTCAAC GGTCCAAAAC 200

AAAAATGCAG CTGCCATTAA AGTCTCAGAT GAACAAACTT CTACACTGAT 250

TTTTAAAATC AAGAATAAGG GCAGCAAGTT TCTGGATTCA CTGAATCAAC 300

AGACACAAAA AGCTGGCAAT ATAGCAACTA TGAAGAGAAA AGCTACTAAT 350

AAAATTAACC CAACGCATAG AAGACTTTTT TTTCTCTTCT AAAAACAACT 400

AAGTAAAGAC TTAAATTTAA ACACATCATT TTACAACCTC ATTTCAAAAT 450

GAAGACTTTT ACCTGGACCC TAGGTGTGCT ATTCTTCCTA CTAGTGGACA 500

CTGGACATTG CAGAGGTGGA CAATTCAAAA TTAAAAAAAT AAACCAGAGA 550

AGATACCCTC GTGCCACAGA TGGTAAAGAG GAAGCAAAGA AATGTGCATA 600

CACATTCCTG GTACCTGAAC AAAGAATAAC AGGGCCAATC TGTGTCAACA 650

CCAAGGGGCA AGATGCAAGT ACCATTAAAG ACATGATCAC CAGGATGGAC 700

CTTGAAAACC TGAAGGATGT GCTCTCCAGG CAGAAGCGGG AGATAGATGT 750

TCTGCAACTG GTGGTGGATG TAGATGGAAA CATTGTGAAT GAGGTAAAGC 800

TGCTGAGAAA GGAAAGCCGT AACATGAACT CTCGTGTTAC TCAACTCTAT 850

ATGCAATTAT TACATGAGAT TATCCGTAAG AGGGATAATT CACTTGAACT 900

TTCCCAACTG GAAAACAAAA TCCTCAATGT CACCACAGAA ATGTTGAAGA 950

TGGCAACAAG ATACAGGGAA CTAGAGGTGA AATACGCTTC CTTGACTGAT 1000

CTTGTCAATA ACCAATCTGT GATGATCACT TTGTTGGAAG AACAGTGCTT 1050

GAGGATATTT TCCCGACAAG ACACCCATGT GTCTCCCCCA CTTGTCCAGG 1100

TGGTGCCACA ACATATTCCT AACAGCCAAC AGTATACTCC TGGTCTGCTG 1150

GGAGGTAACG AGATTCAGAG GGATCCAGGT TATCCCAGAG ATTTAATGCC 1200

ACCACCTGAT CTGGCAACTT CTCCCACCAA AAGCCCTTTC AAGATACCAC 1250

CGGTAACTTT CATCAATGAA GGACCATTCA AAGACTGTCA GCAAGCAAAA 1300

GAAGCTGGGC ATTCGGTCAG TGGGATTTAT ATGATTAAAC CTGAAAACAG 1350

CAATGGACCA ATGCAGTTAT GGTGTGAAAA CAGTTTGGAC CCTGGGGGTT 1400

GGACTGTTAT TCAGAAAAGA ACAGACGGCT CTGTCAACTT CTTCAGAAAT 1450

Figure 4 Page 1 of 3

TGGGAAAATT ATAAGAAAGG GTTTGGAAAC ATTGACGGAG AATACTGGCT 1500

TGGACTGGAA AATATCTATA TGCTTAGCAA TCAAGATAAT TACAAGTTAT 1550

TGATTGAATT AGAAGACTGG AGTGATAAAA AAGTCTATGC AGAATACAGC 1600

AGCTTTCGTC TGGAACCTGA AAGTGAATTC TATAGACTGC GCCTGGGAAC 1650

TTACCAGGGA AATGCAGGGG ATTCTATGAT GTGGCATAAT GGTAAACAAT 1700

TCACCACACT GGACAGAGAT AAAGATATGT ATGCAGGAAA CTGCGCCCAC 1750

TTTCATAAAG GAGGCTGGTG GTACAATGCC TGTGCACATT CTAACCTAAA 1800

TGGAGTATGG TACAGAGGAG GCCATTACAG AAGCAAGCAC CAAGATGGAA 1850

TTTTCTGGGC CGAATACAGA GGCGGGTCAT ACTCCTTAAG AGCAGTTCAG 1900

ATGATGATCA AGCCTATTGA CTGAAGAGAG ACACTCGCCA ATTTAAATGA 1950

CACAGAACTT TGTACTTTTC AGCTCTTAAA AATGTAAATG TTACATGTAT 2000

ATTACTTGGC ACAATTTATT TCTACACAGA AAGTTTTTAA AATGAATTTT 2050

ACCGTAACTA TAAAAGGGAA CCTATAAATG TAGTTTCATC TGTCGTCAAT 2100

TACTGCAGAA AATTATGTGT ATCCACAACC TAGTTATTTT AAAAATTATG 2150

TTGACTAAAT ACAAAGTTTG TTTTCTAAAA TGTAAATATT TGCCACAATG 2200

TAAAGCAAAT CTTAGCTATA TTTTAAATCA TAAATAACAT GTTCAAGATA 2250

CTTAACAATT TATTTAAAAT CTAAGATTGC TCTAACGTCT AGTGAAAAAA 2300

ATATTTTTTA AATTTCAGCC AAATAATGCA TTTTATTTTA TAAAAATACA 2350

GACAGAAAAT TAGGGAGAAA CTTCTAGTTT TGCCAATAGA AAATGTTCTT 2400

CCATTGAATA AAAGTTATTT CAAATTGAAT TTGTGCCTTT CACACGTAAT 2450

GATTAAATCT GAATTCTTAA TAATATATCC TATGCTGATT TTCCCAAAAC 2500

ATGACCCATA GTATTAAATA CATATCATTT TTAAAAATAA AAAAAAACCC 2550

AAAAATAATG CATGCATAAT TTAAATGGTC AATTTATAAA GACAAATCTA 2600

TGAATGAATT TTTCAGTGTT ATCTTCATAT GATATGCTGA ACACCAAAAT 2650

CTCCAGAAAT GCATTTTATG TAGTTCTAAA ATCAGCAAAA TATTGGTATT 2700

ACAAAAATGC AGAATATTTA GTGTGCTACA GATCTGAATT ATAGTTCTAA 2750

TTTATTATTA CTTTTTTTCT AATTTACTGA TCTTACTACT ACAAAGAAAA 2800

AAAAACCCAA CCCATCTGCA ATTCAAATCA GAAAGTTTGG ACAGCTTTAC 2850

AAGTATTAGT GCATGCTCAG AACAGGTGGG ACTAAAACAA ACTCAAGGAA 2900

Figure 4

CTGTTGGCTG TTTTCCCGAT ACTGAGAATT CAACAGCTCC AGAGCAGAAG 2950

CCACAGGGGC ATAGCTTAGT CCAAACTGCT AATTTCATTT TACAGTGTAT 3000

GTAACGCTTA GTCTCACAGT GTCTTTAACT CATCTTTGCA ATCAACAACT 3050

TTACTAGTGA CTTTCTGGAA CAATTTCCTT TCAGGAATAC ATATTCACTG 3100

CTTAGAGGTG ACCTTGCCTT AATATATTTG TGAAGTTAAA ATTTTAAAGA 3150

TAGCTCATGA AACTTTTGCT TAAGCAAAAA GAAAACCTCG AATTGAAATG 3200

TGTGAGGCAA ACTATGCATG GGAATAGCTT AATGTGAAGA TAATCATTTG 3250

GACAACTCAA ATCCATCAAC ATGACCAATG TTTTTCATCT GCCACATCTC 3300

AAAATAAAAC TTCTGGTGAA ACAAATTAAA CAAAATATCC AAACCTCAAA 3350

AAAAA 3355

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Met Lys Thr Phe Thr Trp Thr Leu Gly Val Leu Phe Phe Leu Leu
  1               5                  10                  15

Val Asp Thr Gly His Cys Arg Gly Gly Gln Phe Lys Ile Lys Lys
            20                  25                  30

Ile Asn Gln Arg Arg Tyr Pro Arg Ala Thr Asp Gly Lys Glu Glu
            35                  40                  45

Ala Lys Lys Cys Ala Tyr Thr Phe Leu Val Pro Glu Gln Arg Ile
            50                  55                  60

Thr Gly Pro Ile Cys Val Asn Thr Lys Gly Gln Asp Ala Ser Thr
            65                  70                  75

Ile Lys Asp Met Ile Thr Arg Met Asp Leu Glu Asn Leu Lys Asp
            80                  85                  90

Val Leu Ser Arg Gln Lys Arg Glu Ile Asp Val Leu Gln Leu Val
            95                 100                 105

Val Asp Val Asp Gly Asn Ile Val Asn Glu Val Lys Leu Leu Arg
           110                 115                 120

Lys Glu Ser Arg Asn Met Asn Ser Arg Val Thr Gln Leu Tyr Met
           125                 130                 135

Gln Leu Leu His Glu Ile Ile Arg Lys Arg Asp Asn Ser Leu Glu
           140                 145                 150

Leu Ser Gln Leu Glu Asn Lys Ile Leu Asn Val Thr Thr Glu Met
           155                 160                 165

Leu Lys Met Ala Thr Arg Tyr Arg Glu Leu Glu Val Lys Tyr Ala
           170                 175                 180

Ser Leu Thr Asp Leu Val Asn Asn Gln Ser Val Met Ile Thr Leu
           185                 190                 195

Leu Glu Glu Gln Cys Leu Arg Ile Phe Ser Arg Gln Asp Thr His
           200                 205                 210

Val Ser Pro Pro Leu Val Gln Val Val Pro Gln His Ile Pro Asn
           215                 220                 225

Ser Gln Gln Tyr Thr Pro Gly Leu Leu Gly Gly Asn Glu Ile Gln
           230                 235                 240

Arg Asp Pro Gly Tyr Pro Arg Asp Leu Met Pro Pro Pro Asp Leu
           245                 250                 255

Ala Thr Ser Pro Thr Lys Ser Pro Phe Lys Ile Pro Pro Val Thr
           260                 265                 270

Phe Ile Asn Glu Gly Pro Phe Lys Asp Cys Gln Gln Ala Lys Glu
           275                 280                 285
```

Figure 5

```
Ala Gly His Ser Val Ser Gly Ile Tyr Met Ile Lys Pro Glu Asn
                290                 295                 300

Ser Asn Gly Pro Met Gln Leu Trp Cys Glu Asn Ser Leu Asp Pro
                305                 310                 315

Gly Gly Trp Thr Val Ile Gln Lys Arg Thr Asp Gly Ser Val Asn
                320                 325                 330

Phe Phe Arg Asn Trp Glu Asn Tyr Lys Lys Gly Phe Gly Asn Ile
                335                 340                 345

Asp Gly Glu Tyr Trp Leu Gly Leu Glu Asn Ile Tyr Met Leu Ser
                350                 355                 360

Asn Gln Asp Asn Tyr Lys Leu Leu Ile Glu Leu Glu Asp Trp Ser
                365                 370                 375

Asp Lys Lys Val Tyr Ala Glu Tyr Ser Ser Phe Arg Leu Glu Pro
                380                 385                 390

Glu Ser Glu Phe Tyr Arg Leu Arg Leu Gly Thr Tyr Gln Gly Asn
                395                 400                 405

Ala Gly Asp Ser Met Met Trp His Asn Gly Lys Gln Phe Thr Thr
                410                 415                 420

Leu Asp Arg Asp Lys Asp Met Tyr Ala Gly Asn Cys Ala His Phe
                425                 430                 435

His Lys Gly Gly Trp Trp Tyr Asn Ala Cys Ala His Ser Asn Leu
                440                 445                 450

Asn Gly Val Trp Tyr Arg Gly Gly His Tyr Arg Ser Lys His Gln
                455                 460                 465

Asp Gly Ile Phe Trp Ala Glu Tyr Arg Gly Gly Ser Tyr Ser Leu
                470                 475                 480

Arg Ala Val Gln Met Met Ile Lys Pro Ile Asp
                485                 490 491
```

Figure 5 Page 2 of 2

GGCTCAGAGG CCCCACTGGA CCCTCGGCTC TTCCTTGGAC TTCTTGTGTG 50

TTCTGTGAGC TTCGCTGGAT TCAGGGTCTT GGGCATCAGA GGTGAGAGGG 100

TGGGAAGGTC CGCCGCGATG GGGAAGCCCT GGCTGCGTGC GCTACAGCTG 150

CTGCTCCTGC TGGGCGCGTC GTGGGCGCGG GCGGGCGCCC CGCGCTGCAC 200

CTACACCTTC GTGCTGCCCC CGCAGAAGTT CACGGGCGCT GTGTGCTGGA 250

GCGGCCCCGC ATCCACGCGG GCGACGCCCG AGGCCGCCAA CGCCAGCGAG 300

CTGGCGGCGC TGCGCATGCG CGTCGGCCGC CACGAGGAGC TGTTACGCGA 350

GCTGCAGAGG CTGGCGGCGG CCGACGGCGC CGTGGCCGGC GAGGTGCGCG 400

CGCTGCGCAA GGAGAGCCGC GGCCTGAGCG CGCGCCTGGG CCAGTTGCGC 450

GCGCAGCTGC AGCACGAGGC GGGGCCCGGG GCGGGCCCGG GGGCGGATCT 500

GGGGGCGGAG CCTGCCGCGG CGCTGGCGCT GCTCGGGGAG CGCGTGCTCA 550

ACGCGTCCGC CGAGGCTCAG CGCGCAGCCG CCCGGTTCCA CCAGCTGGAC 600

GTCAAGTTCC GCGAGCTGGC GCAGCTCGTC ACCCAGCAGA GCAGTCTCAT 650

CGCCCGCCTG GAGCGCCTGT GCCCGGGAGG CGCGGGCGGG CAGCAGCAGG 700

TCCTGCCGCC ACCCCCACTG GTGCCTGTGG TTCCGGTCCG TCTTGTGGGT 750

AGCACCAGTG ACACCAGTAG GATGCTGGAC CCAGCCCCAG AGCCCCAGAG 800

AGACCAGACC CAGAGACAGC AGGAGCCCAT GGCTTCTCCC ATGCCTGCAG 850

GTCACCCTGC GGTCCCCACC AAGCCTGTGG GCCCGTGGCA GGATTGTGCA 900

GAGGCCCGCC AGGCAGGCCA TGAACAGAGT GGAGTGTATG AACTGCGAGT 950

GGGCCGTCAC GTAGTGTCAG TATGGTGTGA GCAGCAACTG GAGGGTGGAG 1000

GCTGGACTGT GATCCAGCGG AGGCAAGATG GTTCAGTCAA CTTCTTCACT 1050

ACCTGGCAGC ACTATAAGGC GGGCTTTGGG CGGCCAGACG GAGAATACTG 1100

GCTGGGCCTT GAACCCGTGT ATCAGCTGAC CAGCCGTGGG GACCATGAGC 1150

TGCTGGTTCT CCTGGAGGAC TGGGGGGGCC GTGGAGCACG TGCCCACTAT 1200

GATGGCTTCT CCCTGGAACC CGAGAGCGAC CACTACCGCC TGCGGCTTGG 1250

CCAGTACCAT GGTGATGCTG GAGACTCTCT TTCCTGGCAC AATGACAAGC 1300

CCTTCAGCAC CGTGGATAGG GACCGAGACT CCTATTCTGG TAACTGTGCC 1350

CTGTACCAGC GGGGAGGCTG GTGGTACCAT GCCTGTGCCC ACTCCAACCT 1400

CAACGGTGTG TGGCACCACG GCGGCCACTA CCGAAGCCGC TACCAGGATG 1450

GTGTCTACTG GGCTGAGTTT CGTGGTGGGG CATATTCTCT CAGGAAGGCC 1500

GCCATGCTCA TTCGGCCCCT GAAGCTGTGA CTCTGTGTTC CTCTGTCCCC 1550

TAGGCCCTAG AGGACATTGG TCAGCAGGAG CCCAAGTTGT TCTGGCCACA 1600

CCTTCTTTGT GGCTCAGTGC CAATGTGTCC CACAGAACTT CCCACTGTGG 1650

ATCTGTGACC CTGGGCGCTG AAAATGGGAC CCAGGAATCC CCCCCGTCAA 1700

TATCTTGGCC TCAGATGGCT CCCCAAGGTC ATTCATATCT CGGTTTGAGC 1750

TCATATCTTA TAATAACACA AAGTAGCCAC 1780

```
Met Gly Lys Pro Trp Leu Arg Ala Leu Gln Leu Leu Leu Leu Leu
 1               5                  10                  15

Gly Ala Ser Trp Ala Arg Ala Gly Ala Pro Arg Cys Thr Tyr Thr
            20                  25                  30

Phe Val Leu Pro Pro Gln Lys Phe Thr Gly Ala Val Cys Trp Ser
            35                  40                  45

Gly Pro Ala Ser Thr Arg Ala Thr Pro Glu Ala Ala Asn Ala Ser
            50                  55                  60

Glu Leu Ala Ala Leu Arg Met Arg Val Gly Arg His Glu Glu Leu
            65                  70                  75

Leu Arg Glu Leu Gln Arg Leu Ala Ala Ala Asp Gly Ala Val Ala
            80                  85                  90

Gly Glu Val Arg Ala Leu Arg Lys Glu Ser Arg Gly Leu Ser Ala
            95                  100                 105

Arg Leu Gly Gln Leu Arg Ala Gln Leu Gln His Glu Ala Gly Pro
            110                 115                 120

Gly Ala Gly Pro Gly Ala Asp Leu Gly Ala Glu Pro Ala Ala Ala
            125                 130                 135

Leu Ala Leu Leu Gly Glu Arg Val Leu Asn Ala Ser Ala Glu Ala
            140                 145                 150

Gln Arg Ala Ala Ala Arg Phe His Gln Leu Asp Val Lys Phe Arg
            155                 160                 165

Glu Leu Ala Gln Leu Val Thr Gln Gln Ser Ser Leu Ile Ala Arg
            170                 175                 180

Leu Glu Arg Leu Cys Pro Gly Gly Ala Gly Gly Gln Gln Gln Val
            185                 190                 195

Leu Pro Pro Pro Pro Leu Val Pro Val Val Pro Val Arg Leu Val
            200                 205                 210

Gly Ser Thr Ser Asp Thr Ser Arg Met Leu Asp Pro Ala Pro Glu
            215                 220                 225

Pro Gln Arg Asp Gln Thr Gln Arg Gln Gln Glu Pro Met Ala Ser
            230                 235                 240

Pro Met Pro Ala Gly His Pro Ala Val Pro Thr Lys Pro Val Gly
            245                 250                 255

Pro Trp Gln Asp Cys Ala Glu Ala Arg Gln Ala Gly His Glu Gln
            260                 265                 270

Ser Gly Val Tyr Glu Leu Arg Val Gly Arg His Val Val Ser Val
            275                 280                 285
```

Figure 7

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Trp Cys Glu Gln Gln Leu Glu Gly Gly Gly Trp Thr Val Ile Gln
                290                 295                 300

 Arg Arg Gln Asp Gly Ser Val Asn Phe Phe Thr Thr Trp Gln His
                305                 310                 315

 Tyr Lys Ala Gly Phe Gly Arg Pro Asp Gly Glu Tyr Trp Leu Gly
                320                 325                 330

 Leu Glu Pro Val Tyr Gln Leu Thr Ser Arg Gly Asp His Glu Leu
                335                 340                 345

 Leu Val Leu Leu Glu Asp Trp Gly Gly Arg Gly Ala Arg Ala His
                350                 355                 360

 Tyr Asp Gly Phe Ser Leu Glu Pro Glu Ser Asp His Tyr Arg Leu
                365                 370                 375

Arg Leu Gly Gln Tyr His Gly Asp Ala Gly Asp Ser Leu Ser Trp
                380                 385                 390

His Asn Asp Lys Pro Phe Ser Thr Val Asp Arg Asp Arg Asp Ser
                395                 400                 405

Tyr Ser Gly Asn Cys Ala Leu Tyr Gln Arg Gly Gly Trp Trp Tyr
                410                 415                 420

His Ala Cys Ala His Ser Asn Leu Asn Gly Val Trp His His Gly
                425                 430                 435

Gly His Tyr Arg Ser Arg Tyr Gln Asp Gly Val Tyr Trp Ala Glu
                440                 445                 450

Phe Arg Gly Gly Ala Tyr Ser Leu Arg Lys Ala Ala Met Leu Ile
                455                 460                 465

Arg Pro Leu Lys Leu
                470
```
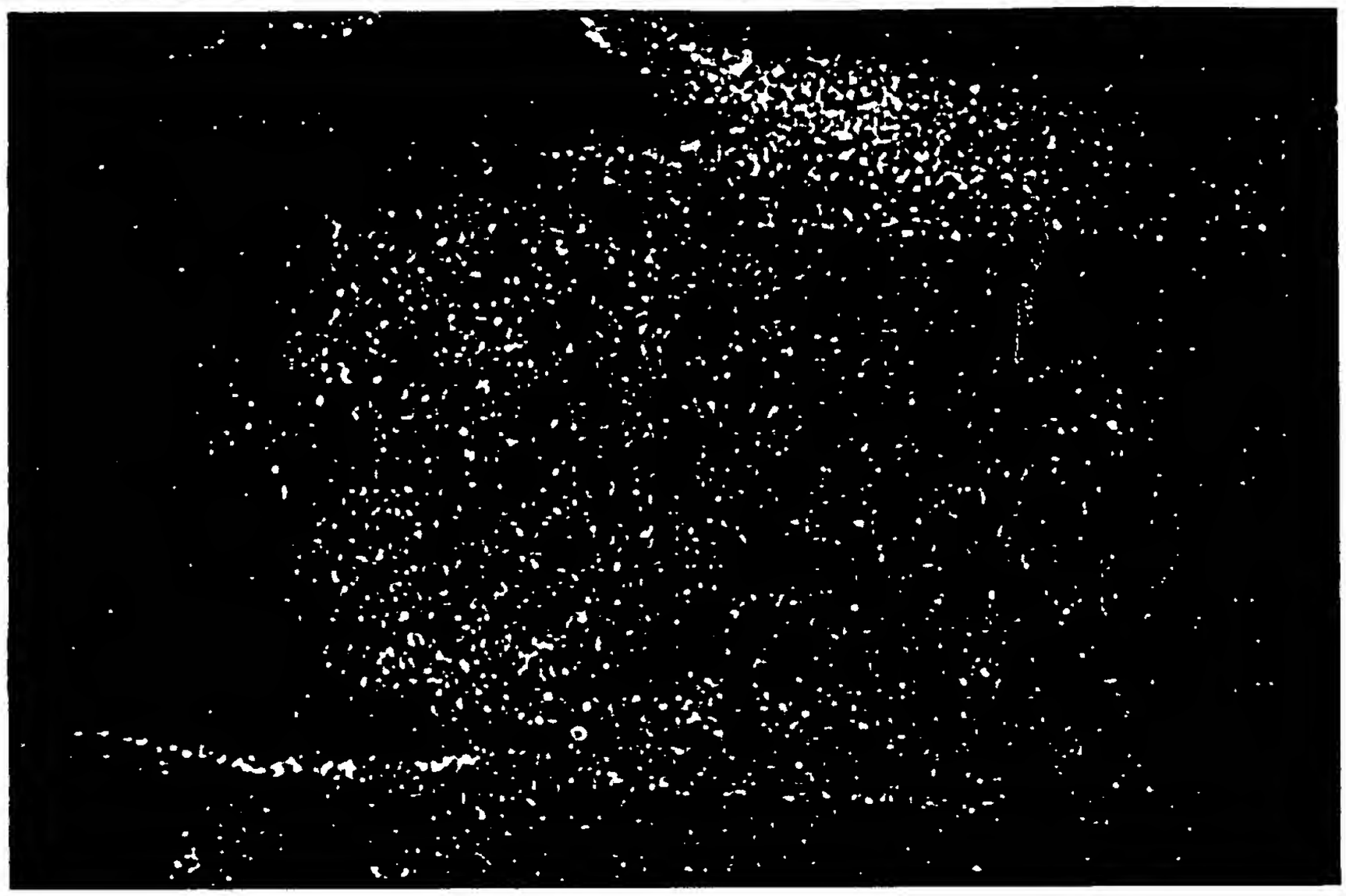

Figure 7 Page 2 of 2

DNA 22779 Dark Field



The white spots represent the silver grains.

Figure 8-A

DNA 22779 H&E

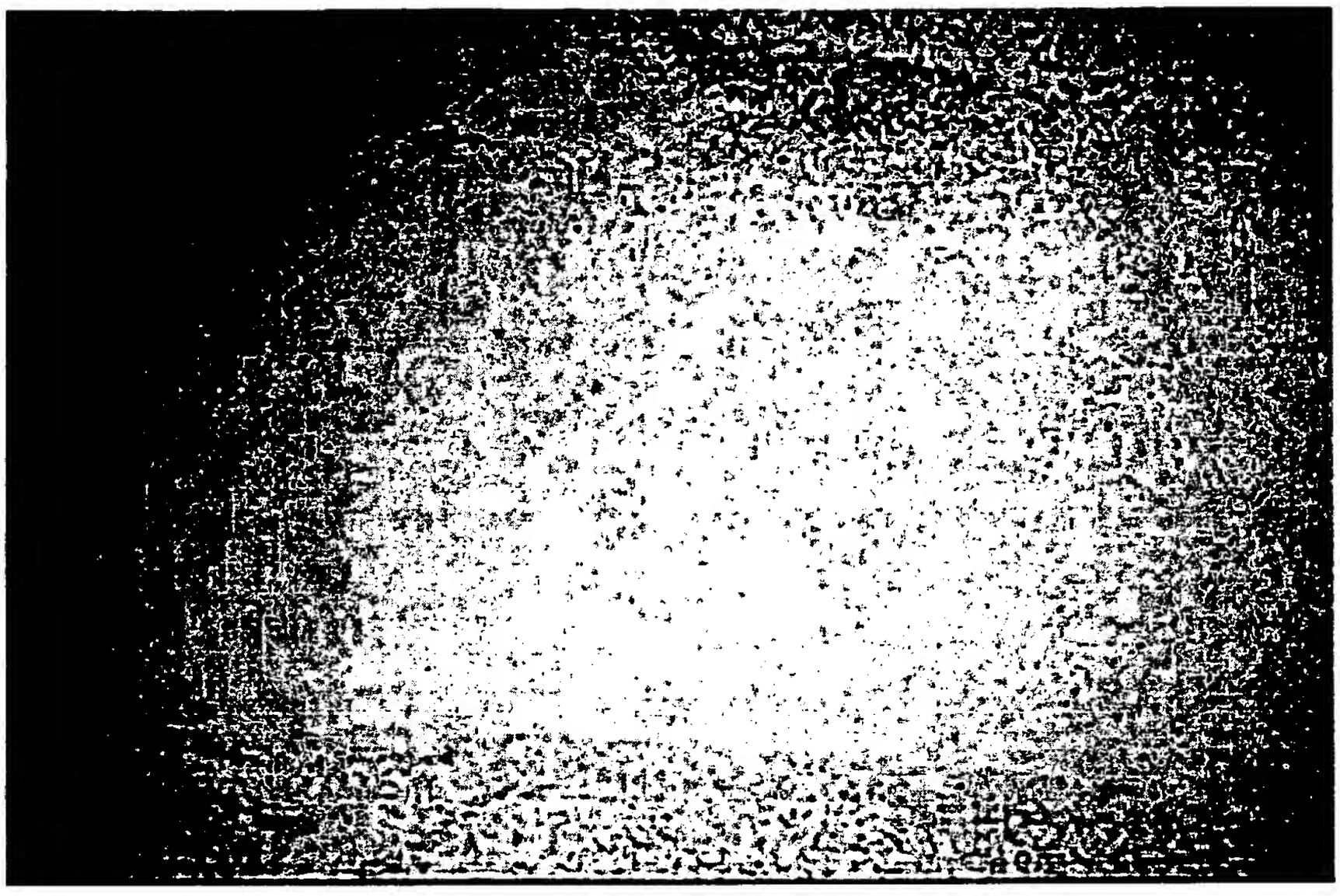


Figure 8-B

DNA 28497 H&E

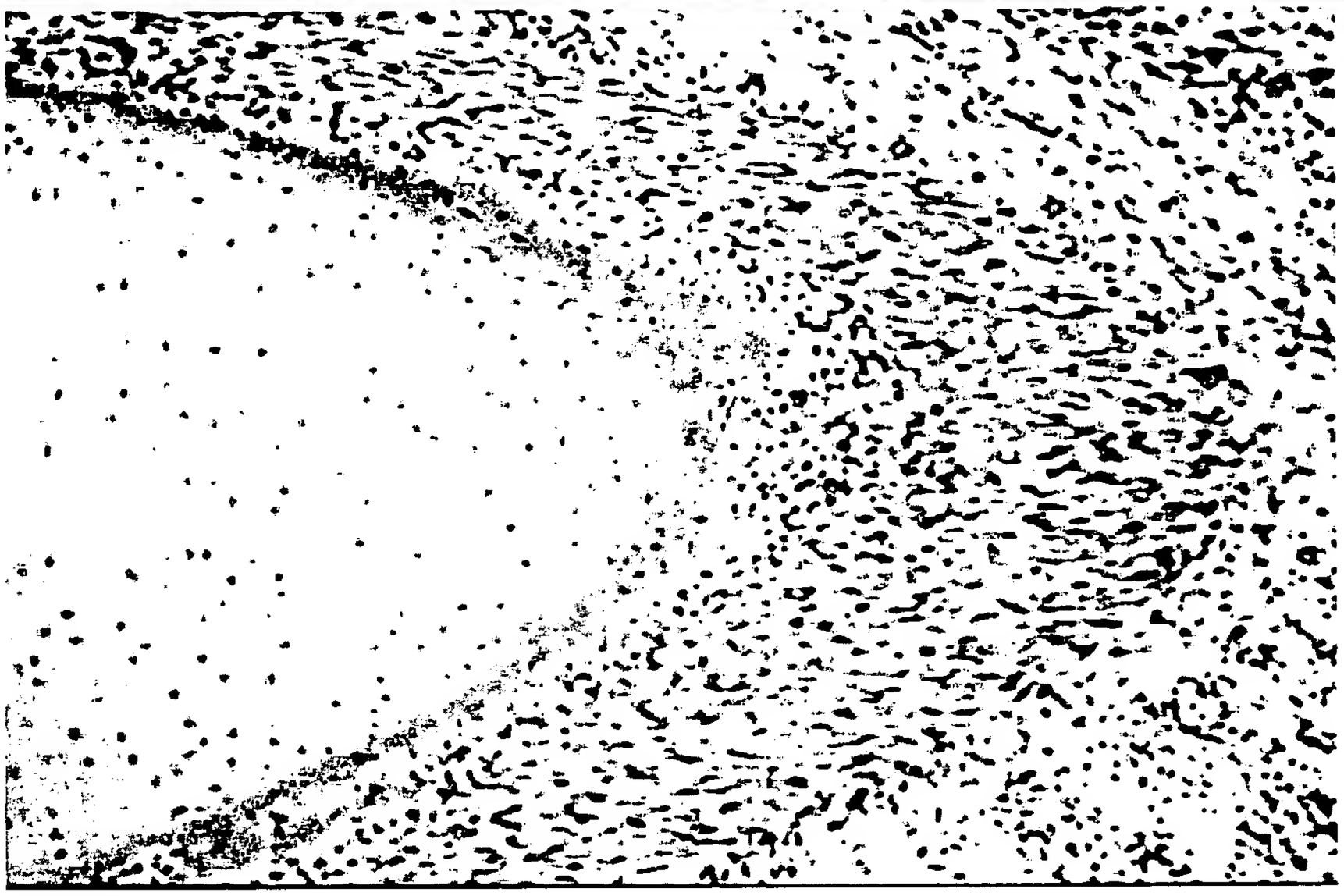
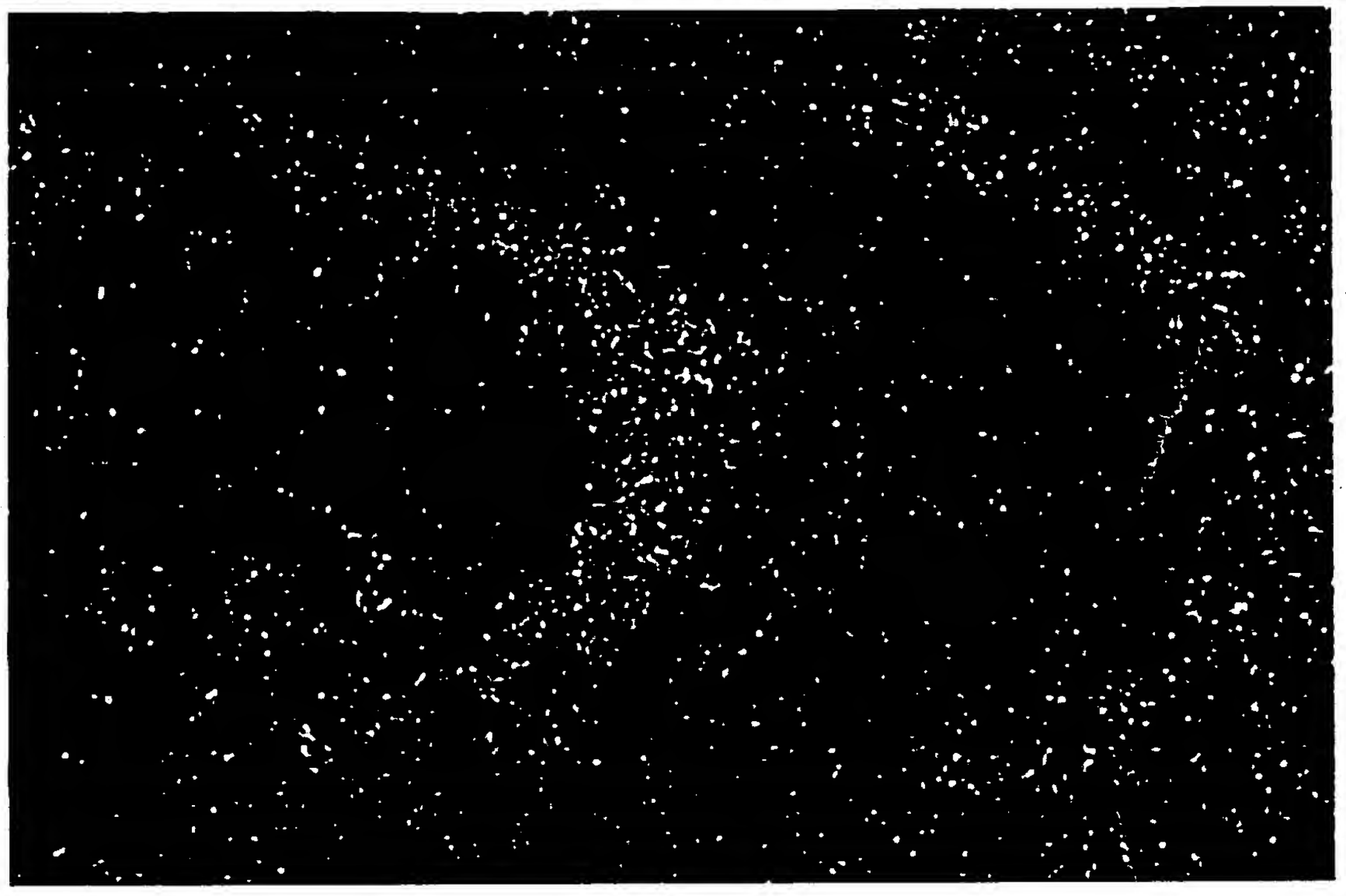


Figure 9A

DNA 28497 Dark Field



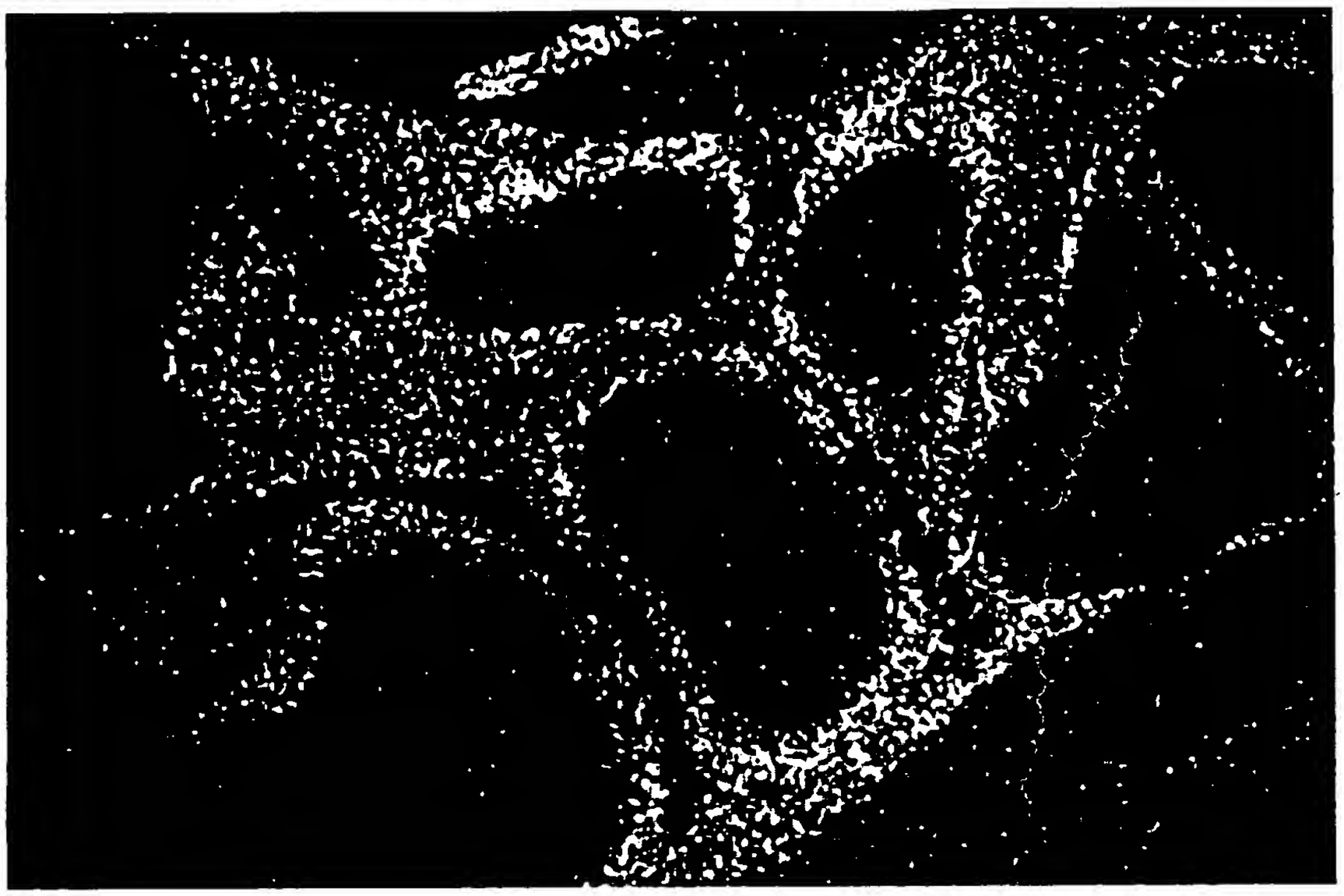
The white spots represent the silver grains.

Figure 9B

DNA 23339 H&E

Figure 10-A

DNA 23339 Dark Field



The white spots represent the silver grains.

Figure 10-B

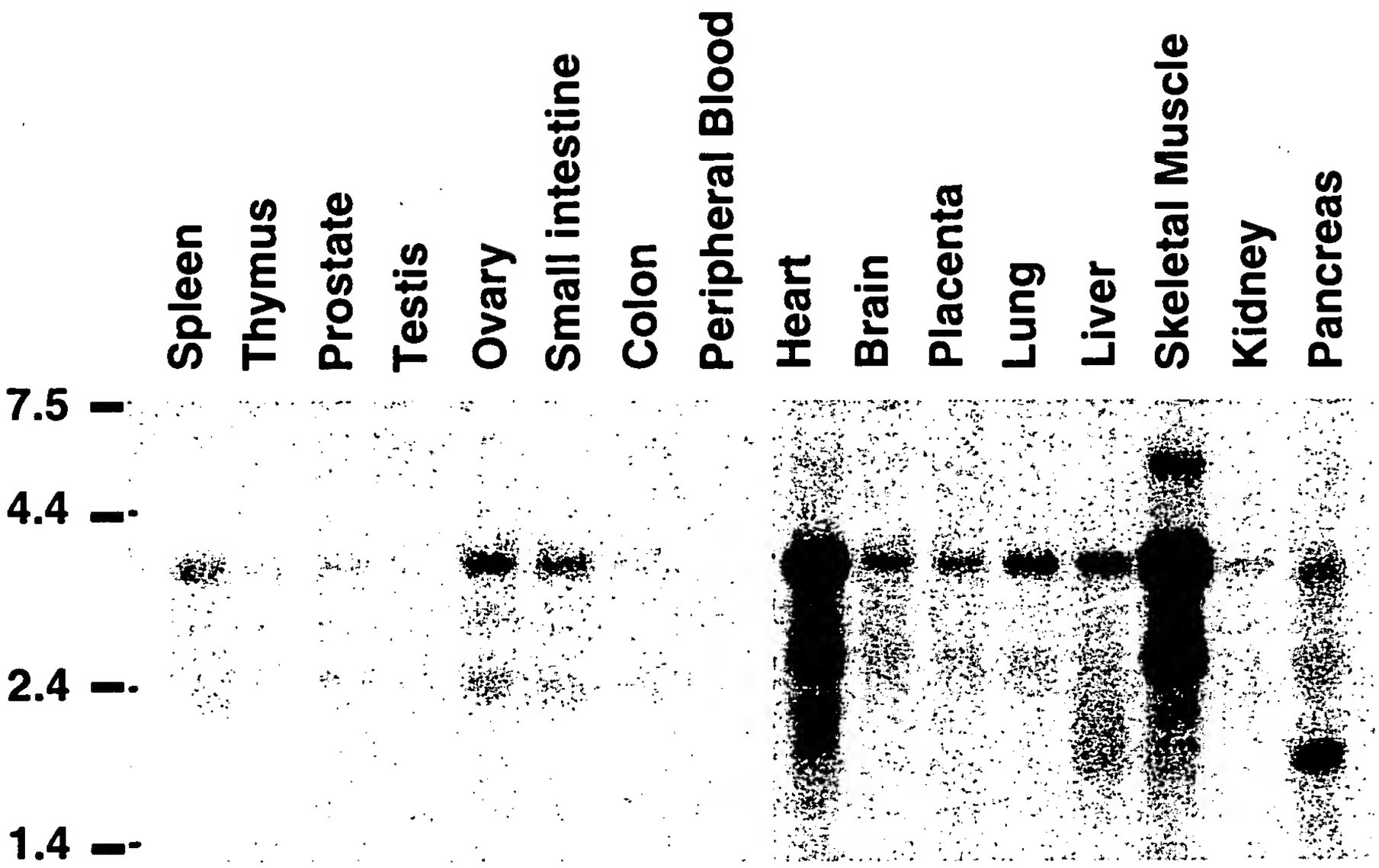

NL1 Northern
Spleen
Thymus
Prostate
Testis
Ovary
Small intestine
Colon
Peripheral Blood
Heart
Brain
Placenta
Lung
Liver
Skeletal Muscle
Kidney
Pancreas
7.5
4.4
2.4
1.4

Figure 11

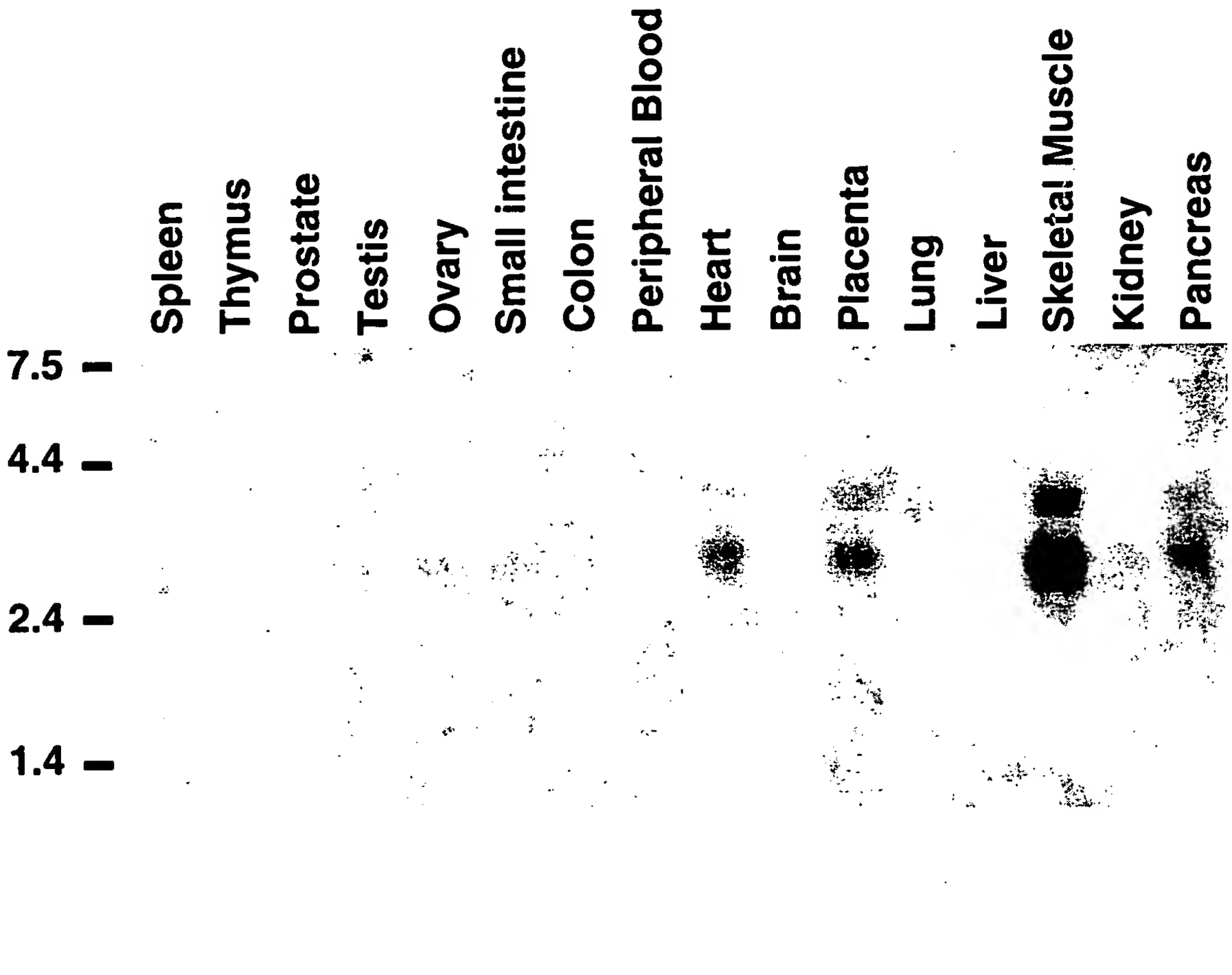

NL5 Northern
Spleen
Thymus
Prostate
Testis
Ovary
Small intestine
Colon
Peripheral Blood
Heart
Brain
Placenta
Lung
Liver
Skeletal Muscle
Kidney
Pancreas
7.5
4.4
2.4
1.4

Figure 12